



OpenAmapthèque

A library management software for scientific and technical information specialists in research units

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ABSTRACT

OpenAmapthèque - Un SIGB libre pour les structures de recherche - Microsoft Internet Explorer

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Recherche simple

Saisissez vos termes de recherche (opérateur booléen ET).

Critères de recherche

Titre ou Nom de journal
Auteur

Affiner la recherche

Année de : à :
Type de document : Tout Langue : Tout

Personnes connectées
1 personne invitée.

	Actuellement	Aujourd'hui	Ce mois-ci	Cette année
Total	1	1	7	24

The Botany and Computational Plant Architecture Joint Research Unit (UMR AMAP) has developed an integrated library management freeware (ILMS), which is distributed under GNU/GPL licence. The software, called OpenAmapthèque, was developed specially for research structures. It is intended for scientific and technical information specialists and non-professionals in charge of managing documentary resources and publications within research units or laboratories.

Free OpenAmapthèque Download :

http://umramap.cirad.fr/amac2/logiciels_amap/index.php?page=openamaptheque

In addition to the usual functions of an ILMS (cataloguing, document circulation management, budget management and OPACs), the OpenAmapthèque system has several advantages:

- Full control of internal publications within research structures (laboratory, unit), covering every type of scientific document
- The possibility of importing and exporting notes in EndNote format
- A personal space for readers: access to loans, management of virtual shelves and personal search profiles, generation of alerts
- Simple software administration within the abilities of library staff
- Easy integration of internal publications into Internet/Intranet portals



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Notice

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Articles

Auteurs: Abu Ahmad, Y.; Royer, M.

Titre: Geographical distribution of four Sugarcane yellow leaf virus genotypes

Année: 2006

Journal: Plant Disease

Volume: 90 Numéro: 9 Pages: 1156-1160

Mots clés

Thématique

Résumé

Specific primer pairs were designed to distinguish four genotypes (BRA for Brazil, CUB for Cuba, PER for Peru, and REU for Réunion Island) of Sugarcane yellow leaf virus (SCYLV) by reverse transcription-polymerase chain reaction (RT-PCR). A unique genome fragment was amplified from each genotype, with the exception of genotypes BRA and PER that are phylogenetically relatively close and were designated genotype BRA-PER. These RT-PCR primers were then used to identify the SCYLV genotype(s) present in 18 different sugarcane growing locations in the world, and 245 leaf samples infected by the virus were analyzed. Most samples were infected by only one of the three genotypes, but mixed infections occurred. Genotype BRA-PER was found in all sugarcane growing locations, whereas genotypes CUB and REU were each found in four geographical locations only. Genotypes BRA-PER, CUB, and REU were all three detected in locally bred sugarcane cultivars in Guadeloupe, indicating local transmission of these genotypes. In contrast, only genotypes BRA-PER and CUB were found in locally bred cultivars in Réunion, whereas genotype REU was detected in this country in cultivar R570 imported from Réunion. Similarly, genotypes BRA-PER and REU are both present in Réunion, but genotype BRA-PER has not, as of yet, spread on this island. Presence of several SCYLV genotypes in Brazil, Colombia, Guadeloupe, Mauritius, and Réunion suggests different virus introductions and/or different evolution histories of the virus after its introduction into a new environment. (Résumé d'auteur)

EXPORTER

Notice abrégée + Résumé

Exporter la notice au format EndNote

Scientific document management : journal articles, books, book sections, conference proceedings, thesis, reports, multimedia materials

KEYWORDS : ILMS, OPAC, GNU/GPL

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